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Amendments to the Claims:

Please cancel claims 8 and 14-33 without disclaimer to prejudice to applicants' right to pursue the subject matter of these claims in a future continuation or divisional application.

Please amend claims 9-13 and add new claims 34-48 as set forth below.

1. (Original) A crystallized complex comprising acyl carrier protein synthase (ACPS) and acyl carrier protein (ACP).
2. (Original) The crystallized complex of Claim 1, wherein ACPS comprises amino acid residues ARG14, MET18, ARG21, GLN22, ARG24, PHE25, ARG28, ARG45, PHE54, GLU58, ILE68, GLY69, ALA70, SER73 and PHE74, or conservative substitutions thereof.
3. (Original) The crystallized complex of Claim 2, wherein ACPS further comprises amino acid residues ASP8, ILE9, THR10, GLU11, LEU12, ILE15, ALA16, SER17, ALA19, GLY20, ALA23, ALA26, GLU27, ILE29, LEU41, SER42, LYS44, GLU48, ALA51, LYS57, SER61, LYS62, THR66, GLY67, GLN71, LEU72, GLN75, ASP76, ILE-77, GLN83, ASN84, LYS93, HIS105, THR106 and ALA107, or conservative substitutions thereof.
4. (Original) The crystallized complex of Claim 1, wherein ACP comprises amino acid residues ARG14, LYS29, ASP35, SER36, LEU37, ASP38, VAL40, GLU41, VAL43, MET44, GLU47, ASP48, ILE54, SER55, ASP56, GLU57 and GLU60, or conservative substitutions thereof.

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5. (Original) The crystallized complex of Claim 4, wherein ACP further comprises amino acid residues ASP13, LEU15, PHE28, GLU30, ASP31, LEU32, GLY33, ALA34, VAL39, LEU42, GLU45, LEU46, GLU49, MET52, GLU53, ASP58, ALA59, and LYS61, or conservative substitutions thereof.

6. (Original) The crystallized complex of Claim 1, characterized as being in rod-shape form with space group C222<sub>1</sub>, and having unit cell parameters of a=78.46 Å, b=122.03 Å and c=136.77 Å.

7. (Original) The crystallized complex of Claim 6, further characterized as including three molecules of ACPS and three molecules of ACP in an asymmetric unit.

8. (Canceled)

9. (Currently amended) An active site of an acyl carrier protein synthase comprising the ~~relative~~ structural coordinates according to Figure 3 and 3A-1 to 3A-79 of amino acid residues ARG14, MET18, ARG21, GLN22, ARG24, PHE25, ARG28, PHE54, GLU58, ILE68, GLY69, ALA70, SER73 and PHE74 from a first monomer of ACPS, and residue ARG45 from a second monomer of ACPS, in each case  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

10. (Currently amended) The active site of Claim 9, further comprising the ~~relative~~ structural coordinates according to Figure 3 and 3A-1 to 3A-79 of amino acid residues ASP8, ILE9, THR10, GLU11, LEU12, ILE15, ALA16, SER17, ALA19, GLY20, ALA23, ALA26, GLU27, ILE29, ALA51, LYS57, SER61, LYS62, THR66, GLY67, GLN71, LEU72, GLN75, ASP76, ILE77 and LYS93 from said first monomer of ACPS and residues

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LEU41, SER42, LYS44, GLU48, GLN83, ASN84, HIS105, THR106 and ALA107 from said second monomer of ACPS, in each case  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

11. (Currently amended) An active site of an acyl carrier protein comprising the relative structural coordinates according to Figure 3 and 3A-1 to 3A-79 or Figure 5 and 5A-1 to 5A-15 of amino acid residues ARG14, LYS29, ASP35, SER36, LEU37, ASP38, VAL40, GLU41, VAL43, MET44, GLU47, ASP48, ILE54, SER55, ASP56, GLU57 and GLU60,  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

12. (Currently amended) The active site of Claim 11, further comprising the relative structural coordinates according to Figure 3 and 3A-1 to 3A-79 or Figure 5 and 5A-1 to 5A-15 of amino acid residues ASP13, LEU15, PHE28, GLU30, ASP31, LEU32, GLY33, ALA34, VAL39, LEU42, GLU45, LEU46, GLU49, MET52, GLU53, ASP58, ALA59, and LYS61,  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

13. (Currently amended) An active site of *B. subtilis* ACP defined by the structural coordinates of Figure 5 and 5A-1 to 5A-15,  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

14-33. (Canceled)

34. (New) The crystallized complex of Claim 1, wherein the crystallized ACPS-ACP complex has the structural coordinates set forth in Figure 3 and 3A-1 to 3A-79,  $\pm$  a

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root mean square deviation from the backbone atoms of the amino acids of not more than 1.5Å.

35. (New) The crystallized complex of Claim 1, wherein ACPS comprises an active site comprising the structural coordinates according to Figure 3 and 3A-1 to 3A-79 of amino acid residues ARG14, MET18, ARG21, GLN22, ARG24, PHE25, ARG28, PHE54, GLU58, ILE68, GLY69, ALA70, SER73 and PHE74 from a first monomer of ACPS, and residue ARG45 from a second monomer of ACPS, in each case  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

36. (New) The crystallized complex of Claim 35, wherein the active site of ACPS further comprises the structural coordinates according to Figure 3 and 3A-1 to 3A-79 of amino acid residues ASP8, ILE9, THR10, GLU11, LEU12, ILE15, ALA16, SER17, ALA19, GLY20, ALA23, ALA26, GLU27, ILE29, ALA51, LYS57, SER61, LYS62, THR66, GLY67, GLN71, LEU72, GLN75, ASP76, ILE77 and LYS93 from said first monomer of ACPS and residues LEU41, SER42, LYS44, GLU48, GLN83, ASN84, HIS105, THR106 and ALA107 from said second monomer of ACPS, in each case  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

37. (New) The crystallized complex of Claim 1, wherein ACP comprises an active site comprising the structural coordinates according to Figure 3 and 3A-1 to 3A-79 of amino acid residues ARG14, LYS29, ASP35, SER36, LEU37, ASP38, VAL40, GLU41, VAL43, MET44, GLU47, ASP48, ILE54, SER55, ASP56, GLU57 and GLU60,  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

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38. (New) The crystallized complex of Claim 37, wherein the active site of ACP further comprises the structural coordinates according to Figure 3 and 3A-1 to 3A-79 of amino acid residues ASP13, LEU15, PHE28, GLU30, ASP31, LEU32, GLY33, ALA34, VAL39, LEU42, GLU45, LEU46, GLU49, MET52, GLU53, ASP58, ALA59, and LYS61,  $\pm$  a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

39. (New) The method of Claim 34, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

40. (New) The method of Claim 39, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

41. (New) The method of Claim 35, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

42. (New) The method of Claim 41, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

43. (New) The method of Claim 36, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

44. (New) The method of Claim 43, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

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45. (New) The method of Claim 37, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

46. (New) The method of Claim 45, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.

47. (New) The method of Claim 38, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 1.0 Å.

48. (New) The method of Claim 47, wherein the  $\pm$  a root mean square deviation from the backbone atoms of said amino acids is not more than 0.5 Å.